

Corrected sequence listing
SEQUENCE LISTING

<110> Consortium fuer elektrochemische Industrie GmbH

<120> Feedback-resistant Homoserine-Transsuccinylases

<130> CO-P#####

<140>

<141>

<160> 12

<170> PatentIn Ver. 2.0

<210> 1

<211> 930

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(930)

<300>

<301> Blattner, F. R.

<302> The complete genome sequence of Escherichia coli K-12.

<303> Science

<304> 277

<305> 5331

<306> 1453-1474

<307> 1997

<400> 1

atg	ccg	att	cgt	gtg	ccg	gac	gag	cta	ccc	gcc	gtc	aat	ttc	ttg	cgt	48
Met	Pro	Ile	Arg	Val	Pro	Asp	Glu	Leu	Pro	Ala	Val	Asn	Phe	Leu	Arg	
1				5					10					15		

gaa	gaa	aac	gtc	ttt	gtg	atg	aca	act	tct	cgt	gcg	tct	ggg	cag	gaa	96
Glu	Glu	Asn	Val	Phe	Val	Met	Thr	Thr	Ser	Arg	Ala	Ser	Gly	Gln	Glu	
			20					25					30			

att	cgt	cca	ctt	aag	gtt	ctg	atc	ctt	aac	ctg	atg	ccg	aag	aag	att	144
Ile	Arg	Pro	Leu	Lys	Val	Leu	Ile	Leu	Asn	Leu	Met	Pro	Lys	Lys	Ile	
		35				40						45				

gaa	act	gaa	aat	cag	ttt	ctg	cgc	ctg	ctt	tca	aac	tca	cct	ttg	cag	192
Glu	Thr	Glu	Asn	Gln	Phe	Leu	Arg	Leu	Leu	Ser	Asn	Ser	Pro	Leu	Gln	
	50					55					60					

gtc	gat	att	cag	ctg	ttg	cgc	atc	gat	tcc	cgt	gaa	tcg	cgc	aac	acg	240
Val	Asp	Ile	Gln	Leu	Leu	Arg	Ile	Asp	Ser	Arg	Glu	Ser	Arg	Asn	Thr	
65				70					75					80		

ccc	gca	gag	cat	ctg	aac	aac	ttc	tac	tgt	aac	ttt	gaa	gat	att	cag	288
Pro	Ala	Glu	His	Leu	Asn	Asn	Phe	Tyr	Cys	Asn	Phe	Glu	Asp	Ile	Gln	
				85					90					95		

gat	cag	aac	ttt	gac	ggg	ttg	att	gta	act	ggg	gcg	ccg	ctg	ggc	ctg	336
Asp	Gln	Asn	Phe	Asp	Gly	Leu	Ile	Val	Thr	Gly	Ala	Pro	Leu	Gly	Leu	
			100					105					110			

gtg	gag	ttt	aat	gat	gtc	gct	tac	tgg	ccg	cag	atc	aaa	cag	gtg	ctg	384
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Corrected sequence listing																
Val	Glu	Phe	Asn	Asp	Val	Ala	Tyr	Trp	Pro	Gln	Ile	Lys	Gln	Val	Leu	
		115					120					125				
gag	tgg	tcg	aaa	gat	cac	gtc	acc	tcg	acg	ctg	ttt	gtc	tgc	tgg	gcg	432
Glu	Trp	Ser	Lys	Asp	His	Val	Thr	Ser	Thr	Leu	Phe	Val	Cys	Trp	Ala	
	130					135					140					
gta	cag	gcc	gcg	ctc	aat	atc	ctc	tac	ggc	att	cct	aag	caa	act	cgc	480
Val	Gln	Ala	Ala	Leu	Asn	Ile	Leu	Tyr	Gly	Ile	Pro	Lys	Gln	Thr	Arg	
	145				150					155					160	
acc	gaa	aaa	ctc	tct	ggc	gtt	tac	gag	cat	cat	att	ctc	cat	cct	cat	528
Thr	Glu	Lys	Leu	Ser	Gly	Val	Tyr	Glu	His	His	Ile	Leu	His	Pro	His	
				165					170					175		
gcg	ctt	ctg	acg	cgt	ggc	ttt	gat	gat	tca	ttc	ctg	gca	ccg	cat	tcg	576
Ala	Leu	Leu	Thr	Arg	Gly	Phe	Asp	Asp	Ser	Phe	Leu	Ala	Pro	His	Ser	
			180					185					190			
cgc	tat	gct	gac	ttt	ccg	gca	gcg	ttg	att	cgt	gat	tac	acc	gat	ctg	624
Arg	Tyr	Ala	Asp	Phe	Pro	Ala	Ala	Leu	Ile	Arg	Asp	Tyr	Thr	Asp	Leu	
		195					200					205				
gaa	att	ctg	gca	gag	acg	gaa	gaa	ggg	gat	gca	tat	ctg	ttt	gcc	agt	672
Glu	Ile	Leu	Ala	Glu	Thr	Glu	Glu	Gly	Asp	Ala	Tyr	Leu	Phe	Ala	Ser	
	210					215					220					
aaa	gat	aag	cgc	att	gcc	ttt	gtg	acg	ggc	cat	ccc	gaa	tat	gat	gcg	720
Lys	Asp	Lys	Arg	Ile	Ala	Phe	Val	Thr	Gly	His	Pro	Glu	Tyr	Asp	Ala	
	225				230					235					240	
caa	acg	ctg	gcg	cag	gaa	ttt	ttc	cgc	gat	gtg	gaa	gcc	gga	cta	gac	768
Gln	Thr	Leu	Ala	Gln	Glu	Phe	Phe	Arg	Asp	Val	Glu	Ala	Gly	Leu	Asp	
				245					250					255		
ccg	gat	gta	ccg	tat	aac	tat	ttc	ccg	cac	aat	gat	ccg	caa	aat	aca	816
Pro	Asp	Val	Pro	Tyr	Asn	Tyr	Phe	Pro	His	Asn	Asp	Pro	Gln	Asn	Thr	
			260					265					270			
ccg	cga	gcg	agc	tgg	cgt	agt	cac	ggt	aat	tta	ctg	ttt	acc	aac	tgg	864
Pro	Arg	Ala	Ser	Trp	Arg	Ser	His	Gly	Asn	Leu	Leu	Phe	Thr	Asn	Trp	
		275					280					285				
ctc	aac	tat	tac	gtc	tac	cag	atc	acg	cca	tac	gat	cta	cgg	cac	atg	912
Leu	Asn	Tyr	Tyr	Val	Tyr	Gln	Ile	Thr	Pro	Tyr	Asp	Leu	Arg	His	Met	
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aat	cca	acg	ctg	gat	taa											930
Asn	Pro	Thr	Leu	Asp												
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<210> 2
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<400> 2
 Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg
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 Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu
 20 25 30

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Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile
35 40 45
Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln
50 55 60
Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr
65 70 75 80
Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln
85 90 95
Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu
100 105 110
Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu
115 120 125
Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala
130 135 140
Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg
145 150 155 160
Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His
165 170 175
Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser
180 185 190
Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu
195 200 205
Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser
210 215 220
Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala
225 230 235 240
Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp
245 250 255
Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr
260 265 270
Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp
275 280 285
Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met
290 295 300
Asn Pro Thr Leu Asp
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<210> 3
<211> 30
<212> DNA
<213> Artificial Sequence

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oligonucleotide	Corrected sequence listing metAfw	
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Corrected sequence listing

<212> DNA
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 <211> 25
 <212> DNA
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 <223> Description of Artificial Sequence: Oligonucleotide
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 nnncagatca cgccatacga tctac 25
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 metAmutrev1; N is a 1:1:1:1: mixture of A, T, C and G
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 nnnggtttga ttgtaactgg tgcg 24
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Corrected sequence listing
metAmutrev2 ; N is a 1:1:1:1: mixture of A, T, C and G

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21